

[illegible]

pct-us02-13994-7.rge

	Query Match	Best Local Similarity	Matches 1956:	Conservative	Mismatches	Indels	Gaps
0y	62	96.3%	97.9%	0	39	3	0
0y	142	96.99%	97.99%	0	39	3	0
0y	2	99.99%	99.99%	0	39	3	0
0y	142	99.99%	99.99%	0	39	3	0
0y	202	99.99%	99.99%	0	39	3	0
0y	122	99.99%	99.99%	0	39	3	0
0y	262	99.99%	99.99%	0	39	3	0
0y	182	99.99%	99.99%	0	39	3	0
0y	321	99.99%	99.99%	0	39	3	0
0y	242	99.99%	99.99%	0	39	3	0
0y	381	99.99%	99.99%	0	39	3	0
0y	302	99.99%	99.99%	0	39	3	0
0y	441	99.99%	99.99%	0	39	3	0
0y	362	99.99%	99.99%	0	39	3	0
0y	420	99.99%	99.99%	0	39	3	0
0y	561	99.99%	99.99%	0	39	3	0
0y	480	99.99%	99.99%	0	39	3	0
0y	621	99.99%	99.99%	0	39	3	0
0y	540	99.99%	99.99%	0	39	3	0
0y	681	99.99%	99.99%	0	39	3	0
0y	600	99.99%	99.99%	0	39	3	0
0y	741	99.99%	99.99%	0	39	3	0
0y	660	99.99%	99.99%	0	39	3	0
0y	801	99.99%	99.99%	0	39	3	0
0y	720	99.99%	99.99%	0	39	3	0

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: July 27, 2002, 06:14:36 ; Search time 47164.5 Seconds

Title:	PCT-US02-13994-12
Perfect score:	2039

Sequence: 1 ccacatccgaagcacaagc.....actgnaattctcaaaaaaaaaa 2039

Scoring table:	IDENTITY_NUC	Consent
	100	100

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : GenBank

```

base :
1:  gb_ba:*
2:  gb_hrg:*
3:  gb_hrg:*
4:  gb_hrg:*
5:  gb_ov:*
6:  gb_ov:*
7:  gb_ph:*
8:  gb_ph:*
9:  gb_pr:*
10: gb_ro:*
11: gb_stb:*
12: gb_stb:*
13: gb_stb:*
14: gb_vl:*
15: en_ba:*
16: en_fun:*
17: en_fun:*
18: en_fun:*
19: en_fun:*
20: en_fun:*
21: en_fun:*
22: en_fun:*
23: en_fun:*
24: en_fun:*
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26: en_fun:*
27: en_fun:*
28: en_fun:*
29: en_fun:*
30: en_fun:*
31: en_fun:*
32: en_fun:*
33: en_fun:*

```

SUMMARIES

Result	Query				
No.	Score	Match	length	DB	ID

					Description

C	1	2010	98.6	2617	9	AB000404	Homo sapi
C	2	1944	95.4	2245	9	BC002755	Homo sapi
C	3	1860	92.7	11112	4	AL163677	Homo sapi
C	4	1031	60.7	17881	2	AL156757	Human DNA
C	5	1031	50.7	17881	2	AL156757	Homo sapi
C	6	1033.6	50.7	178655	2	AL1551035	Human DNA
C	7	947.8	46.5	2512	10	BC021369	Homo sapi
C	8	728	35.7	1622	10	AB000411	Y11091 Mus muscu
C	9	493	24.2	1380	5	AB021807	AB023807 Xenopus l
C	10	493	24.1	1380	5	AB021807	AB023807 Mus muscu
C	11	491	24.1	1380	5	AB021807	Y11092 Mus muscu
C	12	467	22.9	1444	4	AF217772	AF217772 Mus muscu
C	13	411.6	20.2	163014	2	AL657068	AL157656 Homo sap
C	14	410.6	20.1	1337	9	HS803208	AF217777 Homo sap
C	15	410.6	20.1	1564	9	AF217777	AF215532 Homo sap
C	16	364.4	14.9	1149	9	AF215532	BC001843 Homo sap
C	17	364.4	14.9	1149	9	AF215532	BC001843 Homo sap
C	18	278	13.6	632	9	AK001710	AC009783 Rattus no
C	19	262.4	12.9	38636	2	AC009783	AB068675 Sequence
C	20	249	11.8	1607	6	AB086849	AY05405 Drosophil
C	21	209	10.3	3553	3	BM076376	U76376 Drosophil
C	22	209	10.3	3553	3	BM076376	U76376 Drosophil
C	23	202	9.5	406	6	AF292438	AF292438 Human St
C	24	193.4	9.5	406	6	AF292438	AF292438 Human St
C	25	142.2	7.0	10000	2	AC073763	Continuation of
C	26	142.2	7.0	198057	2	AC073763	Continuation of
C	27	137	6.7	164303	2	AC098181	AC098181 Rattus no
C	28	133	6.6	56544	2	AC098181	AC098181 Mus muscu
C	29	127.4	6.2	4222	6	AC026045	AC026045 Homo sap
C	30	96.4	4.7	67932	2	AC018984	AC018984 Drosophil
C	31	96.4	4.7	170324	3	AC007805	AC007805 Drosophil
C	32	96.4	4.7	170324	3	AC007805	250795 Caenorhadr
C	33	99.2	4.7	12012	3	CEB166	AC025360 Homo sap
C	34	88.2	4.3	28256	2	AC025360	AC025360 Homo sap
C	35	76	3.7	285592	2	AC093393	AC093393 Rattus no
C	36	76	3.7	285592	2	AC093393	AC093393 Rattus no
C	37	65.6	3.1	1486	9	AF002833	AF002833 Homo sap
C	38	64	3.1	1486	9	AF002833	AF024237 Homo sap
C	39	61.6	3.0	2422	6	AY056582	AY056582 Sequence
C	40	60.6	3.0	121055	1	NC000474	Y15995 Mouse mRNA
C	41	59.6	2.9	4276	9	AB051552	AB051552 Homo sap
C	42	59.6	2.9	4276	9	AB051552	AB051552 Homo sap
C	43	59	2.9	2590	9	AF080000	AF080000 Homo sap
C	44	59	2.9	3131	6	AX008273	AX008273 Sequence
C	45	59	2.9	3131	6	AX008273	AX008273 Sequence

ALIGNMENTS

RESULT	1
AB000409	AB000409
LOCUS	Homo sapiens mRNA for MNKL complete cds.
DEFINITION	
ACCESSION	AB000409.1 GI:2077824
KEYWORDS	MNKL.
SOURCE	Homo sapiens cell_line:Hela CDNA to mRNA.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes; Metazoa; Chordata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. Fukunaga,R. and Hunter.T.
AUTHORS	Direct Submission
TITLE	Submitted (11-JAN-1997) Rikyo Fukunaga, Osaka University Medical School, Department of Genetics B-3; 2-2 Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:kunugagene@med.osaka-u.ac.jp; Tel:+81-6-879-3318, Fax:+81-6-879-3319)
REFERENCE	Fukunaga,R. and Hunter.T.
AUTHORS	MNKL, a new MAP kinase-activated protein kinase, isolated by a novel expression screening method for identifying protein kinase substrates

Colon cancer ASSOC
Human ORFX ORF27772
Human histone dease
Human full-length
Human histone dease
Human ORFX ORF26059
Human polyucleotide
Caspase 8-interact
Human cDNA sequenc

Dy	2821	cctttaggcttcacatttgatgtttattttttcattcaataaaacaagaagtaaa	2860
Oy	2821	cctttaggcttcacatttgatgtttattttttcattcaataaaacaagaagtaaa	2860
Dy	2881	aatttc 2885	
Oy	2881	aatttc 2885	
Dy	2881	aatttc 2885	
Db	2761	ccaggcgacggagagagccactgatggagcgcgccctctgaccccgcgccecat	2820
RESULT_2			
AC	MAC77217 standard; cDNA, 4021 bp.		
CC	MAC77217;		
CT	MAC77217;		
DT	08-FEB-2001 (first entry)		
DE	Human ORFX ORF2772 polynucleotide sequence SEQ ID NO:5543.		
KM	Human, open reading frame; ORFX; detection: cytotoxic; hepatotropic;		
KM	vulnerability; antisporadic; antiparasitism; neurotropic; neuroprotective;		
KM	anticonsumptive; osteopathic; antihistatic; immunosuppressive; candid;		
KM	immunosilulant; thrombotic; coagulante; vasotropic; antidabetic;		
KM	hypotensive; dermatological; immunosuppressive; antioftalmatory;		
KM	antiviral; antibacterial; antifungal; antineumatic; antichlorid;		
KM	anticancer; gene therapy; cancer; proliferative; antidiarrhoeal;		
KM	neurodegenerative; infectious; diarrheic; antileishmaniasis;		
KM	neurodegenerative disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KM	cholesterol ester storage; systemic lupus erythematosus; infection;		
KM	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KM	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KM	bone damage; catagenesis; antinflammatory disease; coagulation;		
KM	thrombolysis; contraceptive; 88.		
KM	Homo sapiens.		
PX	M0200058473-A2.		
PY	05-OCT-2000.		
PP	31-MAR-2000; 2000MOU-0S08621.		
PR	01-MAR-1999; 99DUS-0127607.		
PR	02-APR-1999; 99DUS-0127636.		
PR	05-APR-1999; 99DUS-0127728.		
PR	30-MAR-2000; 2000OUS-0540763.		
PA	(CDRA -) CORAGEN CORP.		
FJ			
XZ	Shimbetsu Bk., Leach M;		
DR	WPI: 2000-602362/257.		
PT	P-PSDB: AAB41008.		
XX	Novel nucleic acids and peptides derived from open reading frame X,		
XX	useful for treating e.g. cancers, proliferative disorders,		
XX	neurodegenerative disorders and cardiovascular disease -		
XX	Claim 5; Page 4726-4728; 5507pp; English.		
XX	AAC74446 to AAC77606 encodes the proteins given in AAB40237 to AAB43397,		
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX		
CC	sequences have activities such as: cytoskeletal; hepatotropic; vulnary;		
CC	antisporadic; antiparasitism; antidiarrhoeal; antileishmaniasis;		
CC	immunostimulant; candid; thrombotic; coagulative; immunosuppressant;		
CC	antidiabetic; hypocensative; dermatological; immunosuppressive;		
CC	antinflammatory; antibacterial; antiviral; antifungal; antineumatic;		
CC	antichlorid; and anticanceric. The sequences can be used for determining		
OC	the presence of or predisposition to, or preventing or treating		
OC	pathological conditions associated with an ORFX-associated disorder. The		

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OM nucleic - nucleic search, using sw model

Run on: July 27, 2002, 05:37:56 ; Search time 3956.53 Seconds

(Without alignments)
1114.803 Million cell updates/sec

Title: PCT-US02-13994-6

Sequence: IDENTITY NUC

Scoring table: Gapped 10.0, Gapext 1.0

Search: 173646 seqs, 85845221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing limit 45 summaries

Database : N.Corrected_032802.*

1: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1980.DAT.*

2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1981.DAT.*

3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1982.DAT.*

4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1983.DAT.*

5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1984.DAT.*

6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1985.DAT.*

7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1986.DAT.*

8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1987.DAT.*

9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1988.DAT.*

10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1989.DAT.*

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14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1993.DAT.*

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16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1995.DAT.*

17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1996.DAT.*

18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1997.DAT.*

19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1998.DAT.*

20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA1999.DAT.*

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2001.DAT.*

23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2002.DAT.*

24: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the best being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	107.8	99.6	2569	20	AAK0071	Colon cancer assoc
2	63.4	42.0	1265	23	AAK7446	DNA encoding novel
3	53.4	2.1	2750	14	AAK0107	Plasmodium falcipar
4	50.6	2.0	9789	17	AAK1852	GDP coding sequen
5	50.6	1.9	3501	21	AAK0202	DNA encoding plas
6	49.6	1.9	6292	22	AAK6735	Plasmodium falcipa
7	49.6	1.9	2091	21	AAK0115	Plasmodium falcipa
8	48.8	1.9	1452	21	AAK0123	Plasmodium falcipa

10	48.6	1.8	2926	22	AAK1870	cDNA sequence enco
11	47.4	1.8	468	22	AAK0855	Human foetal liver
12	47.4	1.8	468	22	AAK0855	Human foetal liver
13	47.4	1.8	468	22	AAK0855	Human brain expres
14	47.4	1.8	468	22	AAK0855	Human bone marrow
15	47.4	1.8	468	22	AAK0855	Human brain expres
16	47.4	1.8	468	22	AAK0855	Human brain expres
17	47.4	1.8	468	22	AAK0855	Human brain expres
18	47.4	1.8	468	22	AAK0855	Human brain expres
19	47.4	1.8	468	22	AAK0855	Human brain expres
20	47.4	1.8	468	22	AAK0855	Human brain expres
21	47.4	1.8	468	22	AAK0855	Human brain expres
22	47.4	1.8	468	22	AAK0855	Human brain expres
23	47.4	1.8	468	22	AAK0855	Human brain expres
24	47.4	1.8	468	22	AAK0855	Human brain expres
25	47.4	1.8	468	22	AAK0855	Human brain expres
26	47.4	1.8	468	22	AAK0855	Human brain expres
27	47.4	1.8	468	22	AAK0855	Human brain expres
28	47.4	1.8	468	22	AAK0855	Human brain expres
29	47.4	1.8	468	22	AAK0855	Human brain expres
30	47.4	1.8	468	22	AAK0855	Human brain expres
31	47.4	1.8	468	22	AAK0855	Human brain expres
32	47.4	1.8	468	22	AAK0855	Human brain expres
33	47.4	1.8	468	22	AAK0855	Human brain expres
34	47.4	1.8	468	22	AAK0855	Human brain expres
35	47.4	1.8	468	22	AAK0855	Human brain expres
36	47.4	1.8	468	22	AAK0855	Human brain expres
37	47.4	1.8	468	22	AAK0855	Human brain expres
38	47.4	1.8	468	22	AAK0855	Human brain expres
39	47.4	1.8	468	22	AAK0855	Human brain expres
40	47.4	1.8	468	22	AAK0855	Human brain expres
41	47.4	1.8	468	22	AAK0855	Human brain expres
42	47.4	1.8	468	22	AAK0855	Human brain expres
43	47.4	1.8	468	22	AAK0855	Human brain expres
44	47.4	1.8	468	22	AAK0855	Human brain expres
45	47.4	1.8	468	22	AAK0855	Human brain expres

ALIGNMENTS

RESULT 1

AAK0071 standard; DNA: 2569 bp.

XX AAK0071:

02-JUL-1999 (first entry)

DE Colon cancer associated gene.

XX Cancer associated antigen; diagnosis; research; treatment; human.

XX Breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer.

XX Prostate cancer; ss.

XX Homo sapiens.

XX M0904265-A2.

XX 28-JAN-1999.

XX 15-JUL-1998: 98M0-0514679.

XX 22-JUN-1998: 98M0-0102322.

XX 10-OCT-1997: 97M0-0896164.

XX 10-OCT-1997: 97M0-0615999.

XX 10-OCT-1997: 97M0-0061765.

XX 10-OCT-1997: 97M0-0061765.

XX 10-OCT-1997: 97M0-0061765.

XX (LUDM-) LUDMIG INST CANCER RES.

XX Chen Y, Gout I, Gure A, O'Hare M, Odate Y, Old LJ:

Description

```

RESULT      1
MAX40070
ID  MAX40070 standard; DNA; 1087 E
XX

```

LD	AXX40070 standard; DNA; 1087 E
XX	

AC AX40070;
XX

02-JUL-1999 (first entry)
DI
XX

DE
XX

Colon cancer associated gene.

breast cancer; colon cancer; dia

Prostate cancer; 89.
XX

[illegible]

XX

XX

XX 2000 00440 / 2 .
XX 2000 00440 / 2 .

PR 17-JUL-1997; 97US-0896164.

PR 10-OCT-1997; 97US-0061765.

PR 11-OCT-1997; 97GB-0021697.
TY

PA (LUDM-) LUDWIG INST CANCER RES
BY

PI Chen Y, Gout I, Gure A, O'H.

Genome version 4.5
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OK nucleic - nucleic search, using sw model

Run on: July 27, 2002, 05:40:04 : Search time 3956.53 seconds

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Landing first 45 summaries

Title: PCT-US02-13994-10
Sequence: 1 accctccgcagagagcagacgc.....aaagagctcttggaacctt 1953
Scoring table: IDENTITY NTC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 859457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Landing first 45 summaries

Database :
1: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
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7: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2001.DAT.*
23: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*
24: /SIDSL/gcgdata/hold-geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1953	100.0	1953	20	AAAX3673
2	1753	100.0	1953	22	AAAG0280
3	1753	100.0	1953	22	AAAG0280
4	1753	100.0	1953	22	AAAG0280
5	577.6	29.6	5250	22	AAK53315
6	577.6	29.6	5250	22	AAK53315
7	544.8	27.9	3023	24	AAK54958
8	482.4	24.7	549	20	AAK08309
9	482.4	24.7	549	21	AAK09161

10	482.4	24.7	549	22	AAAD3236
11	478	24.5	2543	22	AAAG0279
12	478	24.5	2543	22	AAAG0279
13	478	24.5	2543	22	AAAG0279
14	478	24.5	2543	22	AAAG0279
15	404.8	20.7	416	22	AA129106
16	359	18.4	424	20	AAAG0241
17	359	18.4	424	21	AAAG0241
18	359	18.4	424	21	AAAG0241
19	359	18.4	424	21	AAAG0241
20	305.4	15.6	6568	20	AA15657
21	305.4	15.6	6568	20	AA15657
22	287.6	14.7	338	16	AA131447
23	279.6	14.3	6568	16	AA131446
24	249	12.7	3306	23	AB161531
25	249	12.7	3306	23	AB161531
26	249	12.7	3306	23	AB161531
27	249	12.7	3306	23	AB161531
28	227	11.6	575	22	AAK37320
29	227	11.6	575	22	AAK37320
30	227	11.6	575	22	AAK37320
31	224	11.5	575	22	AAK37320
32	224	11.5	575	22	AAK37320
33	224	11.5	575	22	AAK37320
34	224	11.5	575	22	AAK37320
35	224	11.5	575	22	AAK37320
36	145.6	7.5	238	22	AA152964
37	145.6	7.5	238	22	AA152964
38	137.6	7.0	5250	22	AAK53315
39	137.6	7.0	5250	22	AAK53315
40	137	6.5	2156	20	AAK41301
41	133	6.3	3017	22	AAK57564
42	133	6.3	3017	22	AAK57564
43	123	6.3	2431	22	AAK57538
44	120.6	6.2	2431	22	AAK57538
45	116.9	6.1	511	21	AAAG0823

ALIGNMENTS

RESULT 1	AAAX3673	standard: DNA: 1953 bp.
ID	AAAX3673	
AC	AAAX3673	
XX	02-JUL-1999 (first entry)	
DT		
DX		
XX	Renal cancer associated gene.	
XX	Renal cancer associated antigen; diagnosis; research; treatment; human.	
KW	Breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;	
KW	Prostate cancer; ss.	
XX		
XX	Hom sapiens.	
XX	MO9904265-A2.	
XX	28-JAN-1999.	
XX	15-JUL-1998: 98MO-US14679.	
XX	22-JUN-1998: 98MO-010332.	
XX	17-OCT-1997: 97MO-0896184.	
XX	10-OCT-1997: 97MO-0615599.	
XX	10-OCT-1997: 97MO-0061705.	
XX	11-OCT-1997: 97MO-0021697.	
XX	(UDM-) LUDWIG INST CANCER RES.	
XX	Chen Y, Gout I, Gure A, O'Hare M, Ohta Y, Old LJ:	

[illegible]

